Appl. No.: 10/750,076 Amdt. Dated July 2, 2007 Reply to Office action of April 30, 2007

APPENDIX A

```
ALIGN calculates a global alignment of two sequences
version 2.0 Please cite: Myers and Miller, CABIOS (1989) 4:11-17
IFN-B
                                            166 aa vs.
NO.1
                                            166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
99.4% identity;
                    Global alignment score: 916
            10
                     20
                             30
                                      40
                                              50
                                                       60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
      MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
NO.1
                     20
                             30
            70
                                     100
                     80
                             90
                                             110
                                                      120
ifn b. EMLONIFALFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSL
      NO.1
      EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
            70
                     80
                             90
                                     100
                                             110
                                                      120
           130
                    140
                            150
                                     160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      ..............
NO.1
     HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                    140
                            150
                                     160
IFN-B
                                            166 aa vs.
NO.2
                                            165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
97.0% identity;
                   Global alignment score: 875
                     20
                             30
                                      40
                                              50
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
      NO.2
     MC-NLSQFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
             10
                      20
            70
                             90
                                     100
                     80
                                             110
                                                      120
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
NO.2
     60
             70
                     80
                              90
                                      100
                                              110
           130
                    140
                            150
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
NO.2
    120
            130
                    140
                             1.50
                                      160
TFN-B
                                            166 aa vs.
NO.3
                                            165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
                   Global alignment score: 874
96.4% identity;
```

```
10
                    20
                            30
                                    40
                                             50
                                                     60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     MC-DLPOFLORSSNFOSOKLLWOLNGRLEYCLKDRMNFDIPEEIKOLOOFOKEDAALTIY
NO.3
             10
                     20
                             30
                                     40
            70
                    80
                            90
                                   100
                                            110
                                                    120
ifn b. EMLONIFALFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSL
     NO.3
     EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
     60
             70
                    80
                             90
                                    100
                                            110
           130
                   140
                           150
                                   160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     NO.3
     HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
    120
            130
                    140
                            150
IFN-B
                                          166 aa vs.
                                          165 aa
NO.4
scoring matrix: pam120.mat, gap penalties: -12/-4
97.0% identity;
                   Global alignment score: 878
            10
                    20
                            30
                                    40
                                             50
                                                     60
ifn b. MSYNLLGFLORSSNFOCOKLLWOLNGRLEYCLKDRMNFDIPEEIKOLOOFOKEDAALTIY
     NO.4
     MS-DLPQFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                     20
             10
                             30
                                     40
                                             50
            70
                    80
                            90
                                   100
                                            110
                                                    120
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
     EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
NO.4
             70
                    80
                             90
                                    100
                                            110
           130
                   140
                           150
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
NO.4
    120
            130
                    140
                            1.50
                                    160
IFN-B
                                          166 aa vs.
                                          165 aa
NO.5
scoring matrix: pam120.mat, gap penalties: -12/-4
86.8% identity;
                   Global alignment score: 740
                    20
            10
                             30
                                     40
                                             50
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNG-RLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
            . .: . .:: :..
                            ..........
     MS-DLPE-THSLDNRRTLMLLAQMSRISPEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
NO.5
                     20
             1.0
                              30
                                     40
                                              50
```

```
70
                    80
                             90
                                    100
ifn b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
     YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
NO.5
             70
                     80
                             90
                                     100
           130
                    140
                            150
ifn b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
            130
                    140
                             150
IFN-B
                                         166 aa vs.
NO.6
                                         165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
97.0% identity;
                   Global alignment score: 884
                    20
                                    40
                                            50
            10
                            30
                                                    60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     NO.6
     MC-DLPQFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                    20
            10
                            30
                                    40
                                             50
            70
                    80
                            90
                                   100
                                           110
                                                   120
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
     NO.6
     EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
    60
            70
                    80
                             90
                                    100
                                            110
           130
                   140
                           150
                                   160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
    120
           130
                   140
                            150
                                    160
IFN-B
                                         166 aa vs.
NO.7
                                         166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
88.0% identity;
                   Global alignment score: 824
                    20
                            30
            10
                                    40
                                            50
                                                    60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     ................
NO.7
     MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                    20
                                            50
           10
                            30
                                    40
                                                    60
            70
                    80
                            90
                                   100
                                           110
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
     NO.7
     EMLQNIFALFRQDSSSTGWNEDLPDKFCTELYQQLNDLEACVMQELEKEDFTRGKLMSSL
                   80
            70
                            90
                                   100
                                          110
```

ifn h		130	140	150	160	DNI	
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN ::::::::::::::::::::::::::::::::::::							
NO.7		RILHYLKAK 130	EYSHCAWTIV 140	RVEILRNFYF 150	'INRLTGYL' 160	RN	
		130	140	130	100		
IFN-B						166 aa vs.	
NO.8						166 aa vs.	
	g matrix identity		mat, gap p Global al				
		10	20	30	40	50	60
ifn_b.						KQLQQFQKEDAAI ••••••	
NO.8		FLQRSSNFQ	CQKLLWQLNG	RLEYCLKDRM	NFDIPEEI:	KQLQQFQKEDAAI	TIY
		10	20	30	40	50	60
		70	80	90	100	110	120
ifn_b.						KLEKEDFTRGKLM :::::::::::	
NO.8						ELEKEDFTRGKLM	
		70	80	90	100	110	120
		130	140	150	160		
ifn_b.			EYSHCAWTIV				
NO.8			:::::: EYSHCAWTIV				
		130	140	150	160		
IFN-B						166 aa vs.	
NO.9	a matrix	: pam120.	mat, gap p	enalties:	-12/-4	166 aa	
			Global al				
		10	20	30	40	50	60
ifn_b.						KQLQQFQKEDAAI	
NO.9			~ ~			::::::::: KQLQQFQKEDAAL	
		10	20	30	40	50	60
		70	80	90	100	110	120
ifn_b.						KLEKEDFTRGKLM	
NO.9			::::::: TGWNETIVEN			::::: EERVGETPRGKLM	
1.0.9	2112	70	80	90	100	110	120
		130	140	150	160		
ifn_b.			EYSHCAWTIV			RN	
NO.9	HI KDVVC		:::::: EYSHCAWTIV				
140.5		130	140	150	160	L \ L \ 4	

```
IFN-B
                                           166 aa vs.
NO.10
                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
93.4% identity;
                   Global alignment score: 847
            10
                    20
                             30
                                     40
                                             50
                                                     60
ifn b. MSYNLLGFLORSSNFOCOKLLWOLNGRLEYCLKDRMNFDIPEEIKOLOOFOKEDAALTIY
     NO.10 MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRHDFGFPQEEFDGNQFQKEDAALTIY
                             30
                                     40
                                             50
            70
                    80
                             90
                                    100
                                            110
                                                    120
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      NO.10 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
            70
                    80
                             90
                                    100
                                            110
           130
                   140
                            150
                                    160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     ............
NO.10 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                   140
                            150
                                    160
IFN-B
                                           166 aa vs.
                                           166 aa
NO.11
scoring matrix: pam120.mat, gap penalties: -12/-4
97.0% identity;
                   Global alignment score: 891
            10
                    20
                             30
                                     40
                                             50
                                                     60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     NO.11 MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRHDFGFPEEIKQLQQFQKEDAALTIY
            10
                    20
                             30
                                     40
                                             50
            70
                    80
                             90
                                                     120
                                    100
                                            110
ifn b. EMLONIFALFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSL
     NO.11 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                                    100
            70
                    80
                             90
                                            110
           130
                   140
                            150
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      NO.11 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                   140
                            150
                                    160
IFN-B
                                           166 aa vs.
NO.12
                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
96.4% identity;
                   Global alignment score: 882
```

ifn b.	10 MSYNLLGFLQRSSNFÇ	20 COKLLWOLNGF	30 RLEYCLKDRM	40 NFDIPEEI	50 KOLOOFOKEDAA	60 LTIY
_ NO.12	::::::::::::::::::::::::::::::::::::::	:::::::::	:::::::	::::::	:::::::	::::
	10	20	30	40	50	60
ifn_b.	70 EMLQNIFALFRQDSSS ::::::::::::::::::::::::::::::::::	:::::::::	:::::::	::::::	:::::::::::::::::::::::::::::::::::::::	::::
1.0.11	70	80	90	100	110	120
ifn_b. NO.12	130 HLKRYYGRILHYLKAK :::::::::::::::::::::::::::::::::::	:::::::::	RVEILRNFYF	::::::	::	
IFN-B NO.13					166 aa vs. 166 aa	
	g matrix: pam120. identity;	mat, gap pe Global ali				
ifn_b. NO.13	10 MSYNLLGFLQRSSNFQ ::::::::::::::::::::::::::::::::::::	:::::::::	::::::	.::.:	:::::::	::::
	70	80	90		110	120
_	EMLQNIFALFRQDSSS	TGWNETIVENI	LANVYHQIN	HLKTVLEE	KLEKEDFTRGKL	MSSL
NO.13	EMLQNIFALFRQDSSS 70	TGWNETIVENI 80	PO 90	100	110	120
ifn b.	130 HLKRYYGRILHYLKAK	140 EYSHCAWTIVF	150 RVEILRNFYF	160 INRLTGYL	RN	
NO.13	::::::::::::::::::::::::::::::::::::::					
IFN-B NO.14					166 aa vs. 166 aa	
scoring matrix: pam120.mat, gap penalties: -12/-4 99.4% identity; Global alignment score: 921						
ifn_b.	10 MSYNLLGFLQRSSNFQ					
NO.14	MSYNLLGFLQRSSNFÇ 10	CQKLLWQLNGF 20	RLEYCLKDRM 30	NFGIPEEI 40	KQLQQFQKEDAA 50	LTIY 60

```
70
                    80
                            90
                                    100
                                            110
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      NO.14 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                                            110
            70
                    80
                            90
                                    100
           130
                   140
                           150
                                    160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      ..............
NO.14 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                   140
                           150
IFN-B
                                          166 aa vs.
NO.15
                                          166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
99.4% identity;
                   Global alignment score: 916
            10
                    20
                                     40
                                             50
                            30
                                                     60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     NO.15 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQGQQFQKEDAALTIY
            10
                                             50
                    20
                            30
                                    40
            70
                    80
                            90
                                    100
                                            110
                                                    120
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      NO.15 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
            70
                    80
                            90
                                    100
                                                    120
                                            110
           130
                   140
                           150
                                    160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      .............
NO.15 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                   140
                           150
                                    160
IFN-B
                                          166 aa vs.
                                          166 aa
NO.16
scoring matrix: pam120.mat, gap penalties: -12/-4
98.8% identity;
                   Global alignment score: 911
                            30
            10
                    20
                                     40
                                             50
                                                     60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
      ...... ....
NO.16 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFGIPEEIKQGQQFQKEDAALTIY
                    20
                                             50
            10
                            30
                                     40
                                                     60
            70
                    80
                            90
                                    100
                                            110
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      NO.16 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                            90
                                   100
            70
                    80
                                           110
```

ifn h	13		- -	150	160	7.7.7	
ifn_b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN							
NO.16	HLKRYYGRI:					RN	
	13	0 1	40	150	160		
T D						1.66	
IFN-B NO.17						166 aa 166 aa	VS.
	g matrix:	pam120.ma	t. dap be	nalties: -	-12/-4	100 aa	
				gnment sc			
	_						
	1		20	30	40	50	60
ifn_b.	MSYNLLGFL						
NO 17				TEVOLKDDIII			
NO.17	MSYNLLGFL		20 20	30	40	лунун ул 50	EDAALIII 60
	Τ.	O	20	30	10	50	00
	7	0	80	90	100	110	120
ifn_b.	EMLQNIFAL:	FRQDSSSTG	WNETIVENL	LANVYHQINI	HLKTVLEER	KLEKEDFT	RGKLMSSL
_				:::::::::			
NO.17	~						
	7	0	80	90	100	110	120
	13	∩ 1	.40	150	160		
ifn h	HLKRYYGRI	_	- -			SN	
			:::::::::		:::::::::	:	
NO.17	HLKRYYGRI:	LHYLKAKEY	SHCAWTIVR	VEILRNFYF:	INRLTGYLE	RN	
	13	0 1	40	150	160		
IFN-B						166 aa	110
NO.18						166 aa	V 5 .
	g matrix:	pam120.ma	t, gap pe	nalties: -	-12/-4	100 44	
	identity;						
	_						
	1		20	30	40	50	60
ifn_b.	MSYNLLGFL						
NO 10							
NO.18	MSYNLLGFL		KTTMÖTNGK 50	LEYCLKDRK:	40	лунунук 50	EDAALTIY 60
	Τ.	O	20	30	40	50	00
	7	0	80	90	100	110	120
ifn b.	EMLQNIFAL:	FRQDSSSTG	WNETIVENL			KLEKEDFT	
_	:::::::	::::::::	:::::::	:::::::::	::::::::	::::::	::::::
NO.18	EMLQNIFAL:	FRQDSSSTG		**			
	7	0	80	90	100	110	120
	1 2	∩ 1	40	150	160		
ifn h	13 HLKRYYGRI			150 Vett.bnevet	160 INRITGYLE	ΣΝΙ	
TTII_D.				VETTENETE:			
NO.18	HLKRYYGRI:						
	13			150	160		

```
IFN-B
                                           166 aa vs.
NO.19
                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
93.4% identity;
                   Global alignment score: 844
            10
                    20
                             30
                                     40
                                             50
                                                     60
ifn b. MSYNLLGFLORSSNFOCOKLLWOLNGRLEYCLKDRMNFDIPEEIKOLOOFOKEDAALTIY
     NO.19 MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRHDFGFPGEEFDGNQFQKEDAALTIY
                             30
                                     40
                                             50
            70
                    80
                             90
                                    100
                                            110
                                                    120
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      NO.19 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
            70
                    80
                             90
                                    100
                                            110
           130
                   140
                            150
                                    160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     ............
NO.19 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                   140
                            150
                                    160
IFN-B
                                           166 aa vs.
NO.20
                                           166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;
                   Global alignment score: 860
            10
                    20
                             30
                                     40
                                             50
                                                     60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     NO.20 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRHDFEFPQEEFDDKQFQKEDAALTIY
            10
                    20
                             30
                                     40
                                             50
            70
                    80
                             90
                                    100
                                            110
ifn b. EMLONIFALFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSL
     NO.20 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
            70
                    80
                             90
                                    100
                                            110
           130
                   140
                            150
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      NO.20 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                   140
                            150
                                    160
IFN-B
                                           166 aa vs.
NO.21
                                           165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;
                   Global alignment score: 851
```

```
10
                    20
                            30
                                     40
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
      NO.21 MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRADFKIPMEMTE-KQFQKEDAALTIY
                            30
            10
                    20
                                    40
            70
                    80
                            90
                                   100
                                            110
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
     NO.21 EMLONIFALFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSL
             70
                     80
                             90
                                    100
                                             110
           130
                   140
                           150
                                    160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     NO.21 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
            130
                    140
                            150
IFN-B
                                          166 aa vs.
NO.22
                                          166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
               Global alignment score: 680
80.2% identity;
            1.0
                    20
                             30
                                     40
                                              50
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNG-RLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
     ::::::::: . .: . .:: :...
                            ::.:: .:..: . .::::: : :::
NO.22 MSYNLLGF-HSLDNRRTLMLLAQMSRISPSSCLMDRHDFGFPQEEFDGNQFQKAPAILTI
             10
                     20
                             30
                                     40
                                             50
             70
                     80
                             90
                                    100
                                             110
ifn b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
     NO.22 YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
     60
             70
                     80
                             90
                                     100
            130
                    140
                            150
ifn b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     .....
NO.22 LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
    120
            130
                    140
                            150
IFN-B
                                          166 aa vs.
NO.23
                                          166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.6% identity;
                   Global alignment score: 859
                    20
                            30
                                     40
                                             50
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     NO.23 MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPEEEFDGNQFQKAPAILTIY
                    20
                                    40
            10
                            30
                                            50
```

```
70
                     80
                              90
                                     100
                                              110
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      NO.23 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
             70
                     80
                              90
                                     100
                                              110
            130
                    140
                             150
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      ..............
NO.23 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
            130
                    140
                             150
IFN-B
                                            166 aa vs.
NO.24
                                            166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
94.0% identity;
                    Global alignment score: 856
             10
                     20
                                       40
                                               50
                              30
                                                        60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
      ************** ******************** . .***** * ****
NO.24 MSYNLLGFLQRSSNFQSQKLLWQLNGRLEYCLKDRMNFDIPQEEFDGNQFQKAPAILTIY
                                               50
             10
                     20
                              30
                                      40
             70
                     80
                              90
                                      100
                                              110
                                                       120
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
      NO.24 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
             70
                     80
                              90
                                      100
                                                       120
                                              110
            130
                    140
                             150
                                      160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
      NO.24 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
            130
                    140
                             150
                                      160
IFN-B
                                             166 aa vs.
NO.25
                                             165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
77.2% identity;
                    Global alignment score: 638
                     20
             10
                               30
                                       40
                                                50
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNG-RLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
      : .: : . .: . .:: :..
                                ..... ...... . ...... . ....
NO.25 MC-DLPQF-HSLDNRRTLMLLAQMSRISPSSCLMDRHDFGFPQEEFDGNQFQKAPAILTI
              10
                       20
                               30
                                        40
                                                 50
     60
             70
                      80
                               90
                                      100
                                               110
ifn b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
      NO.25 YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
              70
                                                110
      60
                       80
                               90
                                    100
```

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130 140 150 160
ifn b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     ............
NO.25 LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
    120
        130 140
                       150
TFN-B
                                        166 aa vs.
NO.26
                                        166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
91.7% identity;
                 Global alignment score: 812
           10
                   20
                           30
                                  40
                                            50
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEI--KQLQQFQKEDAALT
     NO.26 MSYNLLGFLQRSSNFQSQKLLWQLNGR--SCLKDRHDFGFPQEEFDGNLQQFQKEDAALT
           10
                   20
                            30
                                   40
     60
                    80
                            90
                                   100
                                           110
             70
ifn b. IYEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMS
     NO.26 IYEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMS
            70
                 80
                        90
                               100
                           150
    120
            130
                    140
                                   160
ifn b. SLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     .............
NO.26 SLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
    120
         130
                140
                           150
IFN-B
                                        166 aa vs.
NO.27
                                        166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
80.2% identity;
                 Global alignment score: 680
                  20
                           30
           10
                                   40
                                           50
ifn b. MSYNLLGFLORSSNFOCOKLLWOLNG-RLEYCLKDRMNFDIPEEIKOLOOFOKEDAALTI
     :::::::: .. : .:: : .. : :::: .:.::: . .::::: : ::::
NO.27 MSYNLLGFHSLDNRRTC-MLLAQMSRISPSSCLMDRHDFGFPQEEFDGNQFQKAPAILTI
           10
                    2.0
                           30
            70
                    80
                           90
                                  100
ifn b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
     NO.27 YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
          70
                  80
                                100
                           90
           130
                  140
                          150
   120
ifn b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     NO.27 LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
       130 140 150
   120
                              160
```

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IFN-B
                                          166 aa vs.
NO.28
                                          166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
85.0% identity;
                   Global alignment score: 737
            10
                    20
                             30
                                      40
                                              50
ifn b. MSYNLLGFLORSSNFOCOKLLWOLNG-RLEYCLKDRMNFDIPEEIKOLOOFOKEDAALTI
     NO.28 MSYNLLGF-HSLDNRRTLMLLAQMSRISPSSCLMDRHDFGFPQEIKQLQQFQKEDAALTI
             10
                             30
                                     40
    60
             70
                     80
                             90
                                     100
                                             110
ifn b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
     NO.28 YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
             70
                             90
    60
                     80
                                    100
                                             110
    120
            130
                    140
                            150
                                     160
ifn b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     ...........
NO.28 LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
            130
                    140
                            150
    120
                                    160
TFN-B
                                          166 aa vs.
NO.29
                                          166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
89.8% identity;
                   Global alignment score: 795
                    20
                            30
                                     40
                                             50
                                                     60
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     NO.29 MSYNLLGFLQRSSNFQSQKLAQMSRISPSSCLMDRHDFGFPQEIKQLQQFQKEDAALTIY
            10
                    20
                            30
                                    40
                                             50
            70
                            90
                    80
                                    100
                                            110
                                                    120
ifn b. EMLONIFALFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSL
     NO.29 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
            70
                    80
                            90
                                    100
                                            110
           130
                   140
                           150
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     NO.29 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                   140
                           150
                                    160
IFN-B
                                          166 aa vs.
NO.30
                                          166 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
95.2% identity;
                  Global alignment score: 869
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10
                   20
                            30
                                    40
ifn b. MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
     NO.30 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEEFDGNQFQKAPAILTIY
                           30
            10
                    20
                                   40
                                           50
            70
                    80
                            90
                                   100
                                           110
ifn b. EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
     NO.30 EMLONIFALFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSL
            70
                   80
                            90
                                   100
                                           110
           130
                   140
                           150
                                   160
ifn b. HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     NO.30 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
           130
                   140
                           150
IFN-B
                                         166 aa vs.
NO.31
                                         165 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
              Global alignment score: 683
81.4% identity;
            1.0
                   20
                            30
                                    40
                                            50
ifn b. MSYNLLGFLQRSSNFQCQKLLWQL-NGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
     NO.31 MSYNLLGFHSLGSRRTC-MLLAOMRKISLFSCLKDRHDFGFPOEEFG-NOFOKAETILTI
           10
                    20
                            30
                                    40
            70
                    80
                            90
                                   100
                                           110
ifn b. YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
     NO.31 YEMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS
     60
             70
                     80
                             90
                                    100
                                            110
           130
                   140
                           150
ifn b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
     .....
NO.31 LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
            130
                    140
                            150
IFN-B
                                         166 aa vs.
NO.32
                                         164 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
77.8% identity;
                  Global alignment score: 629
            10
                   20
                            30
                                    40
ifn b. MSYNLLGFLQRSSNFQCQKLLWQL-NGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI
            NO.32 MC-DLPQTHSLGSRRTC-MLLAQMRKISLFSCLKDRHDFGFPQEEFG-NQFQKAETILTI
                     20
                                     40
            10
                             30
```

	60	70	80	90	100	110		
ifn_b.	YEMLQNIFA	LFRQDSSST(GWNETIVENLL	HNIQHYVNA	HLKTVLEEKLEI	KEDFTRGKLMSS		
	::::::::	:::::::::	:::::::::::::::::::::::::::::::::::::::	:::::::	::::::::	::::::::::		
NO.32	YEMLQNIFA	LFRQDSSST(GWNETIVENLL	HNIQHYVNA	HLKTVLEEKLE	KEDFTRGKLMSS		
	60	70	80	90	100	110		
1.	20 1	30	L40 1	.50	160			
ifn_b. LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN								
:::::::::::::::::::::::::::::::::::::::								
NO.32 LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN								
	120	130	140	150	160			